P-10. The derivation of allelic QTL effect without direct estimation(Abstracts of the International Symposium on Recent Advances in Animal Science(IS-RAAS),Joint meeting of 2^<nd> IS-AS and 3^<rd> IS-IFS)

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P-9 Simultaneous estimation of genetic parameters and heterogeneous variances for production traits of Holstein cattle in Japan

K. Hagiya[a], Y. Atagi[a], T. Shirai[a], M. Suzuki[b]
[a]National Livestock Breeding Center, Fukushima 961-8511, Japan
[b]Department of Food Production Science, Obihiro University of Agriculture and Veterinary Medicine, Obihiro 080-8555, Japan

The purpose of this study is to estimate heritabilities, repeatabilities and heterogeneous variances of herd-year-parity-milking frequency (HYPF) subclass for milk, fat and protein yields of Holstein cattle in Japan. Data were 5,552,004 lactation records from 1st to 5th calving on 2,066,992 Holstein cows between January 1985 and August 2004. The pedigree information containing 2,742,992 animals was also used. A single trait animal model with repeated records included HYPF, region-calving month-year and age as fixed effects. Heritabilities and repeatabilities were assumed homogeneous across HYPF. Heterogeneous variances were assumed in HYPF and corrected applying the autoregressive model. Heritabilities and repeatabilities were simultaneously estimated using Method R. The estimates of genetic parameters with correction of heterogeneous variances were compared with the estimates from the same data without the correction. The parameter estimates with correction of heterogeneous variances estimated from the three subsets were 0.323, 0.305 and 0.266 for heritabilities, and 0.509, 0.494 and 0.478 for repeatabilities of milk, fat, and protein yields, respectively. When heterogeneous variances in HYPF were corrected, the estimates of heritabilities and repeatabilities were higher than those without considering heterogeneous variances. On the other hand, the ratios of permanent environmental variances as well as residual variances on phenotypic variances decreased. The estimated heterogeneous variances had increased gradually across years and the estimates of fat were relatively higher than those of milk and protein.

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Y. Nagamine, O. Sasaki and K. Ishii
National Institute of Livestock and Grassland Science, Ikeno-dai 2, Tsukuba, 305-0901, Japan

The genotypic and allelic effect models are equivalent in terms of QTL detection in a simple additive model, but the QTL allelic model has the advantage of providing direct information for marker-assisted selection. However, allelic matrix is four times as large as genotypic IBD matrix, causing computational problems, especially in genome scans examining multiple positions. Transformation from genotypic to allelic effects, after estimating the genotypic effects with smaller IBD matrix, can solve this problem. We demonstrate the transformation from genotypic to allelic values.

For the QTL genotypic effect model: $\mathbf{y}= \mathbf{X}\boldsymbol{f} + \mathbf{Z}\boldsymbol{u} + \mathbf{Z}\boldsymbol{w} + \boldsymbol{e}$. For the QTL allelic effect model: $\mathbf{y}= \mathbf{X}\boldsymbol{f} + \mathbf{Z}\boldsymbol{u} + \mathbf{ZT}\boldsymbol{v} + \boldsymbol{e}$. In these cases, $\mathbf{X}$ is a design matrix for fixed effects, $\mathbf{Z}$ is an incident matrix relating records in $\boldsymbol{y}$ to the animals, and vectors $\boldsymbol{f}$, $\boldsymbol{u}$, $\boldsymbol{w}$ and $\boldsymbol{e}$ are values for fixed, polygene, QTL genotypic and residual effects, respectively. The sizes of $\boldsymbol{u}$ and $\boldsymbol{w}$ are calculated as $n\times1$ for n individuals. Vector $\boldsymbol{v}$ is the QTL allelic effect having a size of $2n\times1$, and $\mathbf{T}$ is an incident matrix relating each animal to its two allelic effects. The genotypic IBD matrix, $\mathbf{Q}$ (= (1/2) $\mathbf{TGT}'$), can be expressed using the allelic IBD matrix, $\mathbf{G}$, and $\mathbf{T}$ matrices. We can derive $\boldsymbol{v}$ without $\mathbf{G}^{-1}$, therefore $\boldsymbol{v} = \mathbf{GT}'\mathbf{Q}^{-1}$ (1/2) $\boldsymbol{w}$. When allelic effects are simple additive effects and $\mathbf{Q}^{-1}$ and $\mathbf{G}^{-1}$ exist, this transformation can give unique estimators of allelic effects.